

# SEQ SEARCH SUMMARY

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 10:44:48 ; Search time 2673 Seconds  
(without alignments)  
9015.011 Million cell updates/sec

Title: US-09-602-740-1  
Perfect score: 828  
Sequence: 1 gaggagcttcgccacatgga.....gcagcgccagctctaacaag 828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	828	100.0	828	6	AX064875 Sequence
	2	828	100.0	6995	6	AX074270 Sequence
	3	828	100.0	6995	6	AX076272 Sequence
	4	828	100.0	338150	1	AP005278 Corynebac
	5	828	100.0	349980	6	AX127148 Sequence
	6	705	85.1	705	6	AX121829 Sequence
	7	480	58.0	3038	6	AX074275 Sequence
c	8	149.6	18.1	15424	1	AE007019 Mycobacte
c	9	149.6	18.1	40790	1	MTCY493 Z95844 Mycobacteri
	10	134.8	16.3	35881	1	U00013 Mycobacteri
c	11	134.8	16.3	312050	1	MLEPRTN3 AL583919 Mycobacte
	12	104	12.6	1080	6	AX066175 Sequence
	13	84	10.1	960	6	AX074273 Sequence
	14	84	10.1	960	6	AX074278 Sequence
	15	81	9.8	957	6	AX121828 Sequence
c	16	73.2	8.8	331	6	AR128446 Sequence
	17	72.2	8.7	22115	1	SCC22 AL096839 Streptomy
	18	61.2	7.4	137478	2	AP004704 Oryza sat
	19	60.8	7.3	1024	8	AY084434 Arabidops
c	20	60.8	7.3	80367	8	AC012329 Arabidops
c	21	60.8	7.3	129757	8	ATF2K15 AL132956 Arabidops
	22	58.6	7.1	1250	8	AY086161 Arabidops
c	23	58.6	7.1	45529	8	AB016884 Arabidops
	24	57.4	6.9	154029	2	AC120538 Oryza sat
c	25	56.8	6.9	148142	1	D90916 Synechocyst
	26	55.4	6.7	10548	1	AE004417 Vibrio ch
c	27	55.4	6.7	21149	2	AC013910 Drosophil
	28	55.4	6.7	99701	2	AC125292 Drosophil
	29	55.4	6.7	179312	3	AC023745 Drosophil
	30	55.4	6.7	314087	3	AE003484 Drosophil
	31	55.4	6.7	334028	2	AC116537 Drosophil
c	32	54.6	6.6	10195	1	U32737 Haemophilus
c	33	54.2	6.5	132685	2	AP005175 Oryza sat

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 09:05:53 ; Search time 229 Seconds  
(without alignments)  
8142.597 Million cell updates/sec

Title: US-09-602-740-1  
Perfect score: 828  
Sequence: 1 gaggagcttcgccacatgga.....gcagcgccagctctaacaag 828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description
	1	828	100.0	828	22	AAF71360	Corynebacterium gl
	2	828	100.0	6995	22	AAF25332	Nucleotide sequenc
	3	828	100.0	6995	22	AAF29332	C. glutamicum OpcA
	4	828	100.0	349980	22	AAH68529	C glutamicum codin
	5	705	85.1	705	22	AAH66710	C glutamicum codin
	6	480	58.0	3038	22	AAF29319	C. glutamicum OpcA
c	7	149.6	18.1	4411529	22	AAI99682	Mycobacterium tube
	8	104	12.6	1080	22	AAF71023	C. glutamicum SRT
	9	84	10.1	960	22	AAF29320	C. glutamicum OpcA
	10	84	10.1	960	22	AAF29333	C. glutamicum OpcA
	11	81	9.8	957	22	AAH66709	C glutamicum codin
c	12	73.2	8.8	331	21	ABQ62809	Mycobacterium tube
	13	63.4	7.7	53178	23	AAS59543	Propionibacterium
	14	60.8	7.3	1022	21	AAC51469	Arabidopsis thalia
	15	60.8	7.3	1024	21	AAC45134	Arabidopsis thalia
	16	58.6	7.1	1250	21	AAC34656	Arabidopsis thalia
	17	58.6	7.1	1256	21	AAC47798	Arabidopsis thalia
	18	58.6	7.1	1310	21	AAC49386	Arabidopsis thalia
	19	55.4	6.7	732	23	ABL18875	Drosophila melanog
	20	55.4	6.7	2982	23	ABL18874	Drosophila melanog
	21	55.4	6.7	4878	23	ABL04246	Drosophila melanog
	22	54.2	6.5	414	21	AAC98274	Human colon cancer
c	23	53.8	6.5	1010	22	AAI60629	Human polynucleoti
	24	53.8	6.5	1015	22	AAI58843	Human polynucleoti
	25	53.8	6.5	1018	21	AAF21892	Human breast and o
	26	48.2	5.8	6132	21	AAC79584	Virulence gene #4.
	27	47.8	5.8	915	21	AAC41761	Arabidopsis thalia
	28	44.6	5.4	1076	21	AAC49387	Arabidopsis thalia
	29	44.6	5.4	1078	21	AAC35307	Arabidopsis thalia
	30	42	5.1	4966	22	AAS36385	Human cardiovascul
c	31	41.2	5.0	7002	23	ABL09667	Drosophila melanog
c	32	41.2	5.0	10637	23	ABL09666	Drosophila melanog
c	33	41	5.0	6558	21	AAZ45602	cDNA sequence of a
c	34	40.6	4.9	592	21	AAZ93361	Sequence encoding
c	35	40.6	4.9	666	22	AAC84604	Human ZF4 protein
c	36	40.2	4.9	381	23	ABL41662	Nucleotide sequenc
c	37	39.6	4.8	3584	23	ABL07253	Drosophila melanog
c	38	39.6	4.8	13531	23	ABL07252	Drosophila melanog
	39	39.2	4.7	645	17	AAT42476	HuntL4 coding sequ
	40	38.8	4.7	1283	23	AAS85010	DNA encoding novel
	41	38.6	4.7	2853	22	AAI58576	Human polynucleoti
	42	38.6	4.7	2863	22	AAI60362	Human polynucleoti
	43	38.6	4.7	7238	22	AAS36386	Human cardiovascul
	44	38.4	4.6	804	24	ABK48294	Degenerate DNA enc
c	45	38.4	4.6	2224	19	AAV35472	Rat rSK3 coding se

## ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 10:54:19 ; Search time 52 Seconds  
(without alignments)  
4883.238 Million cell updates/sec

Title: US-09-602-740-1  
Perfect score: 828  
Sequence: 1 gaggagcttcgccacatgga.....gcagcgccagctctaacaag 828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	149.6	18.1	4411529	4	US-09-103-840A-1			Sequence 1, Appli
c	2	73.2	8.8	331	4	US-09-060-756-308			Sequence 308, App
	3	40	4.8	2830	4	US-09-221-017B-730			Sequence 730, App
c	4	36.4	4.4	477	4	US-09-135-994-1			Sequence 1, Appli
c	5	36.2	4.4	10348	2	US-08-457-273B-41			Sequence 41, Appl
c	6	36.2	4.4	10348	3	US-08-556-419-13			Sequence 13, Appl
c	7	36.2	4.4	10348	4	US-09-041-886-14			Sequence 14, Appl
c	8	36.2	4.4	10366	1	US-08-246-982A-5			Sequence 5, Appli
c	9	36.2	4.4	10366	1	US-08-453-265-5			Sequence 5, Appli
c	10	35.6	4.3	3819	1	US-07-686-322A-3			Sequence 3, Appli
c	11	35.6	4.3	3819	1	US-08-002-999-3			Sequence 3, Appli
c	12	35	4.2	533	6	5482709-5			Patent No. 5482709

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 11:34:33 ; Search time 58 Seconds  
(without alignments)  
6282.855 Million cell updates/sec

Title: US-09-602-740-1  
Perfect score: 828  
Sequence: 1 gaggagcttcgccacatgga.....gcagcgccagctctaacaag 828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	705	85.1	705	9	US-09-738-626-1745	Sequence 1745, Ap
2	81	9.8	957	9	US-09-738-626-1744	Sequence 1744, Ap
3	54.2	6.5	414	10	US-09-925-299-284	Sequence 284, App
4	42	5.1	4966	10	US-09-764-869-1885	Sequence 1885, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 09:54:28 ; Search time 1967 Seconds  
(without alignments)  
6817.419 Million cell updates/sec

Title: US-09-602-740-1  
Perfect score: 828  
Sequence: 1 gaggagcttcgccacatgga.....gcagcgccagctctaacaag 828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					ID	Description
	No.	Score	Match	Length	DB		
	1	72.4	8.7	594	14	BQ250641	BQ250641 TaE25002B
	2	70.8	8.6	476	10	BE415351	BE415351 MWL028.C0
	3	70.8	8.6	490	10	BE443267	BE443267 WHE1110_C
	4	70.8	8.6	533	10	BE443748	BE443748 WHE1122_G
	5	70.8	8.6	568	10	BE444985	BE444985 WHE1130_C
	6	70.8	8.6	578	10	BE443954	BE443954 WHE1123_D
	7	70.8	8.6	636	14	BQ805048	BQ805048 WHE3562_C
	8	70.2	8.5	665	14	BM815572	BM815572 EST593666
	9	68.6	8.3	455	12	BG653158	BG653158 sad82f05.
	10	68.6	8.3	601	14	BQ629730	BQ629730 sap92g05.
	11	67.8	8.2	807	14	BQ804658	BQ804658 WHE3557_C
c	12	67.4	8.1	693	10	AW348678	AW348678 GM210003A
	13	67.4	8.1	1264	10	BE420690	BE420690 HWM001.E0
c	14	67	8.1	713	13	BJ263815	BJ263815 BJ263815
c	15	66	8.0	571	10	BE443356	BE443356 WHE1112_B
	16	66	8.0	648	13	BJ304570	BJ304570 BJ304570
	17	66	8.0	667	13	BJ280131	BJ280131 BJ280131
c	18	66	8.0	681	13	BJ310981	BJ310981 BJ310981
c	19	66	8.0	701	17	BH535842	BH535842 BOGOD15TF
	20	66	8.0	787	12	BF259503	BF259503 HVSMEf001
	21	66	8.0	796	17	BH694649	BH694649 BOHVR23TR
	22	65.6	7.9	477	9	AU084921	AU084921 AU084921
c	23	65	7.9	654	10	BE444903	BE444903 WHE1129_E
	24	64.2	7.8	585	10	AV916596	AV916596 AV916596
	25	64.2	7.8	590	10	AV914327	AV914327 AV914327
	26	64.2	7.8	633	13	BJ472540	BJ472540 BJ472540
	27	64.2	7.8	654	12	BG415469	BG415469 HVSMEk000
	28	64.2	7.8	846	10	BE420795	BE420795 HWM002.F0
c	29	63.8	7.7	683	10	AV919353	AV919353 AV919353
c	30	63.8	7.7	706	13	BJ474639	BJ474639 BJ474639
	31	63.6	7.7	616	12	BF267119	BF267119 HV_CEd001
	32	63.6	7.7	662	14	BQ403858	BQ403858 GA_Ed006
c	33	63	7.6	571	13	BM074416	BM074416 MEST86-A0
c	34	63	7.6	601	13	BM078290	BM078290 MEST117-F
c	35	63	7.6	722	13	BM348739	BM348739 MEST300-B
	36	63	7.6	1316	11	AY105837	AY105837 Zea mays
	37	62.8	7.6	530	10	AV917228	AV917228 AV917228
	38	62.8	7.6	546	10	AV917189	AV917189 AV917189
c	39	62.8	7.6	630	10	AV919939	AV919939 AV919939
c	40	62.8	7.6	685	10	AV922395	AV922395 AV922395
	41	61.6	7.4	805	13	BI311601	BI311601 EST531335
	42	61.4	7.4	531	10	AV940134	AV940134 AV940134
	43	61.4	7.4	626	13	BI780260	BI780260 EBma08_SQ
	44	61.2	7.4	581	10	BE194056	BE194056 HVSMEh008
c	45	61	7.4	293	14	BQ703295	BQ703295 946107G07

# ALIGNMENTS